We claim:

1. A method for the biological production of polyhydroxyalkanoates containing 3-hydroxyhexanoate comprising synthesizing the polyhydroxyalkanoate in a transgenic organism having at least one transgene encoding an enzyme selected from the group consisting of PHB polymerase, PHA polymerase, ß-ketothiolase, ß-ketoacyl-CoA reductase, D-specific enoyl-CoA hydratase, crotonase, butyryl-CoA dehydrogenase, and 3-hydroxybutyryl-CoA dehydrogenase integrated into the chromosome.

2. The method of claim 1 wherein the organism is a bacteria or plant.

3. The method of claim 2 wherein the organism is a plant selected from the group consisting of oil crop plants and starch accumulating plants.

4. The method of claim 3 wherein the plant is selected from the group consisting of Brassica, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.

5. The method of claim 2 wherein the organism is a bacteria selected from the group consisting of *Escherichia, Klebsiella, Ralstonia, Alcaligenes, Pseudomonas,* and *Azotobacter*.

6. The method of claim 1 wherein the organism is genetically engineered to express or overexpress a PHA polymerase incorporating C_6 substrates.

7. The method of claim 6 wherein the enzyme is derived from *Aeromonas caviae, Comamonas testosteroni, Thiocapsia pfenigii, Chromatium vinosum, Bacillus cereus, Nocardia carolina, Nocardia salmonicolor, Rhodococcus ruber, Rhodcoccus rhodocrous,* and *Rhodospirilum rubrum*.

8. The method of claim 1 wherein the organisms are genetically engineered to redirect metabolites to production of 3-hydroxyhexanoyl-CoA.

9. The method of claim 8 wherein the organisms are genetically engineered using a D-specific enoyl-CoA hydratase gene.

10. The method of 9 wherein the hydratase gene is isolated from a bacteria selected from the group consisting of *R. eutropha, Klebsiella aerogenes, P. putida,* and *Aeromonas caviae.*

11. The method of claim 8 wherein the organisms are genetically engineered using a butyrate fermentation pathway.

12. The method of claim 11 wherein the butyrate fermentation pathway is from *Clostridium acetobutylicium* or *Thermoanaerobacterium thermosaccharolyticum.*

13. The method of claim 11 wherein the organisms are genetically engineered to convert butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.

14. The method of claim 11 wherein the organisms are genetically engineered to express a broad range reductase that is active on C_6 substrates.

15. The method of claim 11 wherein the organisms are genetically engineered to express a polymerase that accepts 3-hydroxyhexanoyl CoA.

16. The method of claim 11 wherein the organisms are genetically engineered to express a thiolase accepting acetoacetyl CoA.

17. The method of claim 11 wherein the organisms are genetically engineered to express an enzyme selected from the group consisting of thiolases specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, PHA polymerase that accepts 3-hydroxybutyryl CoA and 3-hydroxyhexanoyl CoA.

18. The method of claim 8 wherein the organisms are genetically engineered using fatty acid biosynthetic enzymes.

19. The method of claim 18 wherein the fatty acid biosynthetic enzymes are enzymes converting acyl ACP to acyl CoA.

20. The method of claim 19 where the enzymes are selected from the group consisting of ACP-CoA transacylase, acyl ACP thioesterase, and acyl CoA synthase.

21. The method of claim 20 wherein the enzymes are acyl ACP thioesterase and acyl CoA synthase.

22. The method of claim 18 wherein the enzymes are derived from *E. coli*.

23. The method of claim 8 wherein the organisms are genetically engineered using a fatty acid oxidation complex.

24. The method of claim 23 wherein the fatty acid oxidation complex comprises enzymes selected from the group consisting of enzymes epimerizing S-3 hydroxyhexanoyl CoA and enzymes reducing 3-ketohexanoyl CoA.

25. The method of claim 24 wherein the enzymes are derived from *Nocardia salmonicolor*.

26. The method of claim 24 wherein the enzymes for epimerization are derived from *Pseudomonas putida* FaoAB complex.

27. The method of claim 23 wherein the organism that is genetically engineered accumulates 3-ketohexanoyl CoA due to a lack of a thiolase.

28. A method for producing polyhydroxybutyrate-co-3-hydroxyhexanoate comprising feeding an organism

butyrate or butanol, and

another feedstock selected from the group consisting of glucose, sucrose, lactose, xylose, methanol, and combinations thereof.

29. A method for producing 3-hydroxyhexanoate copolymers comprising

identifying an organism capable of taking up butyrate and converting it to butyryl-CoA,

fermenting the organism in the presence of butyrate such that PHBH is produced, and

recovering the PHBH.

30. A method for producing 3-hydroxyhexanoate copolymers comprising

identifying bacteria capable of taking up butanol and converting it to butyryl-CoA,

fermenting the organism in the presence of butanol such that PHA is produced, and

recovering the PHA.

31. A genetically engineered organism for use in any of the methods of claims 1-30.

32. The organism of claim 31 wherein the organism is a bacteria.

33. The organism of claim 31 wherein the organism is a higher order plant.

34. A polyhydroxybutyrate-co-3-hydroxyhexanoate produced in a genetically engineered *Escherichia coli* K12.